

AMENDMENTS TO THE SPECIFICATION

Please insert the following section heading and paragraph on page 1, before line 5:

Cross-Reference to Related Applications

The present application is a 35 U.S.C. § 371 National Stage patent application of International patent application PCT/JP04/10459, filed on July 23, 2004, which claims priority to Japanese patent application JP 2003-279156, filed on July 24, 2003, and Japanese patent application JP 2003-412053, filed on December 10, 2003.

Please amend the paragraph beginning on page 12, line 23, as follows:

The fusion monomer can be represented by the formula (SEQ ID NO: 5) (I):



in which X represents the B subunit monomer residue, Y1 and Y2 are each independently peptide bonds or amino acid sequences of up to 4 amino acid residues, Z represents the amino acid sequence of the epitope, and n is 2, 3, or 4. Preferably, Y1 is leucine (L), and Y2 denotes the amino acid residues glutamic acid-isoleucine (EI).

Please amend the paragraph beginning on page 21, line 7, as follows:

A sequence encoding a hinge region was inserted downstream of the CTB gene. A sequence GPGP (SEQ ID NO: 6) between CTB and JEV EIII in the fusion protein can reduce the intermolecular interaction between both protein portions. This effectively functions for forming a pentamer of CTB. Thus, the fusion protein is formed into a pentamer and acquires a GM1-ganglioside-binding property. Since glycine (G) has the smallest side chain (H) in 20 different amino acids and proline (P) has the amino group and the carboxyl group at a right angle, they are suitable as the hinge.

Please amend the paragraph beginning on page 21, line 17, as follows:

E. coli XL-1 Blue strain was transformed by electroporation using a plasmid DNA, and ampicillin-resistant strain was selected with LB-Amp medium. A plasmid vector was isolated from the ampicillin-resistant strain, and DNA sequencing was carried out using a DNA sequencer (AGT ATG GCA AAT (SEQ ID NO: 7)-[CTB]-GGC CCC GGT CCA (SEQ ID NO: 8)-[GPGP (SEQ ID NO: 6) (linker)]-GAA TTC-[EcoRI]-ACC TAT GGC ATG (SEQ ID NO: 9)-[JEV EIII domain N'-terminal sequence]). The DNA base sequence is shown by SEQ ID NO: 2, and the amino acid sequence induced from the nucleotide sequence is shown by SEQ ID NO: 1. In SEQ ID NO: 2, the 1st to 372nd base sequence is derived from CTB, the 373rd to 384th base sequence is the linker, the 385th to 390th base sequence is EcoRI site, and the 391st to 882nd base sequence is JEV EIII domain N'-terminal sequence.

Please incorporate the attached Sequence Listing beginning on new page 31.